In the claims:

For the convenience of the Examiner, all claims being examined are presented below. Please cancel claim 2 without prejudice.

1. **(Amended)** A method for identifying an inhibitor compound capable of reducing the interaction between a first region and a second region, comprising:

a) placing in contact:

i) a potential inhibitor compound;

ii) a first region which is a fragment of a nuclear protein, wherein the fragment comprises a signature motif B^1XXLL, in which B^1 is any natural hydrophobic amino acid, L is leucine, and X independently represents any natural amino acid, and the signature motif is a structural element of a nuclear protein that binds to a liganded nuclear receptor in the process of activating or repressing target genes, and the nuclear protein is a bridging factor responsible for an interaction between a liganded nuclear receptor transcription factor and a transcription initiation complex involved in regulation of gene expression; provided that a fragment that includes residues 624-1287 of TIF-2 is excluded;

iii) a second region which is a liganded nuclear receptor transcription factor or a fragment thereof, wherein the fragment comprises that part of the nuclear receptor transcription factor which is capable of interacting with a nuclear protein through binding to the signature motif; and

b) detecting the presence or absence of inhibition of the interaction between ii) and iii).

3. **(Amended)** A method according to claim 23, wherein B^1 is leucine or valine.

4. **(Amended)** A method according to claim 3, wherein B^1 is leucine.

5. **(Amended)** A method according to claim 1, 3, 4, or 23, wherein the signature motif is B^2B^1XXLL, wherein B^2 is a hydrophobic amino acid.

6. **(Amended)** A method according to claim 5, wherein B^2 is selected from isoleucine, leucine, methionine, phenylalanine, tryptophan, tyrosine and valine.

7. **(Amended)** A method according to claim 1, 3, 4, or 23, wherein the nuclear protein is a coactivator.

8. **(Amended)** A method according to claim 7, wherein the coactivator is selected from RIP 140, SRC-1, TIF2, CBP, p300, TIF1, Trip1, Trip2, Trip3, Trip4, Trip5, Trip8, Trip9, p/CIP, ARA70 & Trip230.

9. **(Amended)** A method according to claim 1, 3, 4, or 23, wherein the transcription factor is a steroid hormone receptor.

10. **(Amended)** A method according to claim 9, wherein the steroid hormone receptor is selected from oestrogen receptor, progesterone receptor, androgen receptor and glucocorticoid receptor.

11. **(Amended)** A method according to claim 10, wherein the steroid hormone receptor is oestrogen receptor.

12. **(Amended)** A method according to claim 1, 3, 4, or 23, wherein the method is a 2-hybrid assay.

13 **(Amended)** A method according to claim 1, 3, 4, or 23, wherein the potential inhibitor compound is a member of a peptide library based on the signature motif.

Please add the following new claim:

23. **(New)** A method according to claim 1, wherein the fragment of a nuclear protein comprises only one signature motif.

The amended claims are restated below to reflect changes from the last filing.

1. **(Amended)** A method for identifying an inhibitor compounds capable of reducing the interaction between a first region and a second region, comprising:

a) placing in contact:

i) a potential inhibitor compound;

ii) a first region which is a fragment of ~~signature motif on~~ a nuclear protein, wherein the fragment comprises a signature motif B^1XXLL, in which B^1 is any natural hydrophobic amino acid, L is leucine, and X independently represents any natural amino acid, and the signature motif is a structural element of a nuclear protein that binds to a liganded nuclear

receptor in the process of activating or repressing target genes. and the nuclear protein is a bridging factor responsible for an interaction between a liganded nuclear receptor transcription factor and a transcription initiation complex involved in regulation of gene expression; provided that a fragment that includes residues 624-1287 of TIF-2 is excluded;

[b)] iii) a second region which is a liganded nuclear receptor transcription factor or a fragment thereof, wherein the fragment comprises that part of the ~~a~~ nuclear receptor which is capable of interacting with the nuclear protein through binding to the signature motif; [~~,~~]and ~~wherein:~~

~~the nuclear protein is a bridging factor that is responsible for the interaction between a liganded nuclear receptor and a transcription initiation complex involved in regulation of gene expression;~~

~~the nuclear receptor is a transcription factor;~~

~~the signature motif is a short sequence of amino acid residues which is the key structural element of a nuclear protein which binds to a liganded nuclear receptor as part of the process of the activation or repression of target genes; and~~

~~in which the method comprises taking:~~

~~i) the potential inhibitor compound;~~

~~ii) the liganded nuclear receptor or a fragment thereof in which the fragment comprises the second region defined in this claim in b) above;~~

iii) ~~a fragment comprising a signature motif of the nuclear protein; and~~

b) detecting the presence or absence of inhibition of the interaction between ii) and iii).

3. **(Amended)** A method according to claim 23 ~~2 or claim 5~~, wherein ~~in which~~ B^1 is leucine or valine.

4. **(Amended)** A method according to claim 3, wherein ~~in which~~ B^1 is leucine.

5. **(Amended)** A method according to claim 1, 3, 4, or 23 wherein ~~in which~~ the signature motif is B^2B^1XXLL wherein B^2 is a~~ny natural~~ hydrophobic amino acid~~, B^2 is a hydrophobic amino acid, L is leucine and X independently represents any natural amino acid~~.

6. **(Amended)** A method according to claim 5, wherein ~~in which~~ B^2 is selected from ~~the group consisting of~~ isoleucine, leucine, methionine, phenylalanine, tryptophan, tyrosine and valine.

7. **(Amended)** A method according to any one of claims 1, 3, 4, or 23 ~~and 5~~, wherein ~~in which~~ the nuclear protein is a coactivator.